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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Jakobsen, Brent Karsten
Gao, George Fu
Gerth, Ulrich Conrad
Sewell, Andrew Kelvin

(ii) TITLE OF INVENTION: CD8 AS AN INHIBITOR OF THE CELLULAR IMMUNE SYSTEM

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Hale and Dorr LLP
(B) STREET: 60 State Street
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: United States
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/560,494
(B) FILING DATE: 28-APR-2000
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/GB98/03235
(B) FILING DATE: 28-OCT-1998

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9722779.7
(B) FILING DATE: 28-OCT-1997

(viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 102286.413

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GACTGAGTCG CGGCCGCTGC CACCATGGCC TTACCAGTGA CCGCCTTG 48

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TATTCGACTG GATCCTTATA CGTATCTCGC CGAAAGGCTG GG 42

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGAATTCCAT ATGAGCCAGT TCCGGGTGTC GCCGCTGGAT CG 42

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

A1 cont

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CGCGGATCCC TATGCGCCCC CCGCTGGCCG GCTCGCCTCT GGGCGCAGGG ACAG 54

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CACCGCGAAT TCGGATCCTA AGCGGGTCTA CAAGCTTCGG GCTTCGCTGG CAGGAAGACC 60

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CACCGCGAAT TCGGATCCTA AGCGGGTCTA CAAGCTTCTG GCGTCGTGGT GGGCTTCGC 59

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

A1 Cont

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CACCGCGAAT TCGGATCCTA AGCGGGTCTA CAAGCTTCGG GCTTCGCTGG CAGGAAGACC 60

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GTGGCAAGCT TGGATCCTAT GGCGTCGTGG TGGGCTTCGC TG 42

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGAATTCCAT ATGAGTCAAT TTCGTGTATC ACCGCTGGAT CG 42

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

A1 cont

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ACATACCCAT GGGCTCTCAC TCCATGAGGT ATTTC 35

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ACATACAAGC TTACGGCTCC CATCTTAAGG TGAGGGGCTT GGG 43

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ile Leu Lys Glu Pro Val His Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

A1 cont

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Ser Leu Tyr Asn Thr Val Ala Thr Leu
1 5

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Val Ile Tyr Gln Tyr Met Asp Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTGTCCAACC CGACGTCGGG CAGCTCGTGG CTCTTCCAGC CG 42

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA prmer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CGGCTGGAAG AGCCACGAGC TGCCCGACGT CGGGTTGGAC AG 42

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGGGGAAGCT TAATGCCATT CGATTTTCTG AGCTTCAAAA ATATCGTTCA GACCACCACC 60

GGATCCTGGC GTCGTGGTGG GCTTCGCTGG CAGGAAGAC 99

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Gly Ser Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
1 5 10 15

Trp His

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA prmer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GAGGAGGAGC ATATGAAACC ACAAGCACCT GAACTACGAA TCTTTCCAAA GAAAATGGAC 60

GCC 63

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGGGAGGGAA GCTTACTTGG TAGTAGTAGA GTTCAC 36

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Lys Ala Val Tyr Asn Phe Ala Thr Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "A synthetic DNA construct encoding part of the extracellular domain of human CD8alpha"

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```
ATG AGT CAA TTT CGT GTA TCA CCG CTG GAT CGG ACC TGG AAC CTG GGC        48
Met Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr Trp Asn Leu Gly
  1               5                  10                  15

GAG ACA GTG GAG CTG AAG TGC CAG GTG CTG CTG TCC AAC CCG ACG TCG        96
Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser
             20                  25                  30

GGC TGC TCG TGG CTC TTC CAG CCG CGC GGC GCC GCC GCC AGT CCC ACC       144
Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr
         35                  40                  45

TTC CTC CTA TAC CTC TCC CAA AAC AAG CCC AAG GCG GCC GAG GGG CTG       192
Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu
     50                  55                  60

GAC ACC CAG CGG TTC TCG GGC AAG AGG TTG GGG GAC ACC TTC GTC CTC       240
Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu
 65                  70                  75                  80

ACC CTG AGC GAC TTC CGC CGA GAG AAC GAG GGC TAC TAT TTC TGC TCG       288
Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser
                 85                  90                  95

GCC CTG AGC AAC TCC ATC ATG TAC TTC AGC CAC TTC GTG CCG GTC TTC       336
Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe
            100                 105                 110

CTG CCA GCG AAG CCC ACC ACG ACG CCA TAG                              366
Leu Pro Ala Lys Pro Thr Thr Thr Pro  *
        115                 120
```

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
Met Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr Trp Asn Leu Gly
  1               5                  10                  15
```

```
Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser
             20                  25                  30

Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr
         35                  40                  45

Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu
     50                  55                  60

Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu
 65                  70                  75                  80

Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser
                 85                  90                  95

Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe
            100                 105                 110

Leu Pro Ala Lys Pro Thr Thr Thr Pro  *
        115                 120
```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "A synthetic DNA construct encoding part of the extracellular domain of murine CD8alpha"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:4..396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
CAT ATG AAA CCA CAA GCA CCT GAA CTA CGA ATC TTT CCA AAG AAA ATG        48
    Met Lys Pro Gln Ala Pro Glu Leu Arg Ile Phe Pro Lys Lys Met
            125                 130                 135

GAC GCC GAA CTT GGT CAG AAG GTG GAC CTG GTA TGT GAA GTG TTG GGG        96
Asp Ala Glu Leu Gly Gln Lys Val Asp Leu Val Cys Glu Val Leu Gly
        140                 145                 150

TCC GTT TCG CAA GGA TGC TCT TGG CTC TTC CAG AAC TCC AGC TCC AAA       144
Ser Val Ser Gln Gly Cys Ser Trp Leu Phe Gln Asn Ser Ser Ser Lys
    155                 160                 165
```

```
CTC CCC CAG CCC ACC TTC GTT GTC TAT ATG GCT TCA TCC CAC AAC AAG       192
Leu Pro Gln Pro Thr Phe Val Val Tyr Met Ala Ser Ser His Asn Lys
170                 175                 180                 185

ATA ACG TGG GAC GAG AAG CTG AAT TCG TCG AAA CTG TTT TCT GCC ATG       240
Ile Thr Trp Asp Glu Lys Leu Asn Ser Ser Lys Leu Phe Ser Ala Met
                190                 195                 200

AGG GAC ACG AAT AAT AAG TAC GTT CTC ACC CTG AAC AAG TTC AGC AAG       288
Arg Asp Thr Asn Asn Lys Tyr Val Leu Thr Leu Asn Lys Phe Ser Lys
            205                 210                 215

GAA AAC GAA GGC TAC TAT TTC TGC TCA GTC ATC AGC AAC TCG GTG ATG       336
Glu Asn Glu Gly Tyr Tyr Phe Cys Ser Val Ile Ser Asn Ser Val Met
        220                 225                 230

TAC TTC AGT TCT GTC GTG CCA GTC CTT CAG AAA GTG AAC TCT ACT ACT       384
Tyr Phe Ser Ser Val Val Pro Val Leu Gln Lys Val Asn Ser Thr Thr
    235                 240                 245

ACC AAG CCA TAA GCTT                                                 400
Thr Lys Pro  *
250
```

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```
Met Lys Pro Gln Ala Pro Glu Leu Arg Ile Phe Pro Lys Lys Met Asp
  1               5                  10                  15

Ala Glu Leu Gly Gln Lys Val Asp Leu Val Cys Glu Val Leu Gly Ser
             20                  25                  30

Val Ser Gln Gly Cys Ser Trp Leu Phe Gln Asn Ser Ser Ser Lys Leu
         35                  40                  45

Pro Gln Pro Thr Phe Val Val Tyr Met Ala Ser Ser His Asn Lys Ile
     50                  55                  60

Thr Trp Asp Glu Lys Leu Asn Ser Ser Lys Leu Phe Ser Ala Met Arg
 65                  70                  75                  80

Asp Thr Asn Asn Lys Tyr Val Leu Thr Leu Asn Lys Phe Ser Lys Glu
                 85                  90                  95
```

```
Asn Glu Gly Tyr Tyr Phe Cys Ser Val Ile Ser Asn Ser Val Met Tyr
           100                 105                 110

Phe Ser Ser Val Val Pro Val Leu Gln Lys Val Asn Ser Thr Thr Thr
       115                 120                 125

Lys Pro  *
    130
```